

RESULT 1
 AA142913 LOCUS 572 bp mRNA linear EST 14-MAY-1997
 DEFINITION z140e07.s1 Soares_pregnant_uterus_NbHPV Homo sapiens CDNA clone
 IMAGE:504420 3', mRNA sequence.
 ACCESSION AA142913
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 572)
 AUTHORS Haller, S., Lennon, G., Becker, M., Donaldo, M.F., Chiapelli, B.,
 Clissoe, J., Dietrich, N., Dubugue, T., Favello, A., Gish, W., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M. B., Tan, F., Thierry-Mieg, J., Trevasaks, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
 TITLE Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL MEDLINE
 COMMENT 97044478
 CONTACT: Wilson RK

Wed Jun 4 11:54:05 2003

us-09-873-

```

IMAGE Consortium (info@image.llnl.gov) <for further information
Insert Length: 1212      Std Error: 0.00
Seq primer: -40M13 fwd. from Amerham
High quality sequence stop: 442.
Location/Qualifiers
1..572

```

```

source
1. .572
/organism="Homo sapiens"
/db_xref="GDB:3809408"
/db_xref="taxon:9606"
/clone_image="504420"
/clone_lib=" Soares_pregnant_uterus_NbHPV"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: uterus; Vector: PT73-Pac; Site.1: Not I;
Site.2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dAT) primer [5' strand cDNA was primed with a Not I -
AATCGAAGAAGATTCGCGCCGCCCTTTTTTTTTTTTTTTTTT 3'] ,
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia) , digested with Not I and cloned into the Not I
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."
191 a 87 c 96 g 198 t

```

Query Match	Similarity	100.0%	Score 572;	DB 9;	Length 572;
Best Local	Similarity	100.0%	Pred. No. 6.5e-94;		
Matches 572;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1	TTTTTGGACATTGCTCTACTGTTTATTATACACGCGTGAATTCACAAGTTTGCTAATGAT	60		
Db	1	TTTTTGGACATGTGCTCTACTGTTTATTATACACGCGTGAATTCACAAGTTTGCTAATGAT	60		
OY	61	ACACAGTCACACCTACCTATATTAATTAATCTCACAGTGTTTTAACTGATGACTTTGTT	120		
Db	61	ACACAGTCACACCTACCTATATTAATTAATCTCACAGTGTTTTAACTGATGACTTTGTT	120		
OY	121	TCAATATTTTAAATAAATTAATTAATGAGGTAAATTCACACAAATGATGAAAGTTTGAG	180		
Db	121	TCAATATTTTAAATAAATTAATTAATGAGGTAAATTCACACAAATGATGAAAGTTTGAG	180		
OY	181	GCATGTCGACAAAATAGTGCAAAAGCCTTAAGTTATCCAAAAGATGATGATCATTAATTA	240		
Db	181	GCATGTCGACAAAATAGTGCAAAAGCCTTAAGTTATCCAAAAGATGATGATCATTAATTA	240		
OY	241	TAAACACTGTGTAGTGTCCCTGGGAAATGCTTACAAATGAGATTCACACAGCAGTCAAAACGG	300		
Db	241	TAAACACTGTGTAGTGTCCCTGGGAAATGCTTACAAATGAGATTCACACAGCAGTCAAAACGG	300		
OY	301	AATCTAACACGACACTGTACAGTAGTACCAAAAGGTATTACAAAAGCTGTCTCGCATGA	360		
Db	301	AATCTAACACGACACTGTACAGTAGTACCAAAAGGTATTACAAAAGCTGTCTCGCATGA	360		
OY	361	ACACGTTAAATAGTCACACATACACAAAGCATACATGCTGTCTGGATTTCGACATG	420		
Db	361	ACACGTTAAATAGTCACACATACACAAAGCATACATGCTGTCTGGATTTCGACATG	420		
OY	421	TTTGTCTTTCTCTCTTAAATATATATTTGGTTATGTGTATATGTTATTTTGTATAA	480		
Db	421	TTTGTCTTTCTCTCTTAAATATATATTTGGTTATGTGTATATGTTATTTTGTATAA	480		
OY	481	AATAAATTCAGAGAAACATCTCTATTTAGACAAAGAAAATGCGAGAAATCTAGATAT	540		
Db	481	AATAAATTCAGAGAAACATCTCTATTTAGACAAAGAAAATGCGAGAAATCTAGATAT	540		
OY	541	TTTCCCTCTTATGGCCGATTAATTTGGTTAC	572		
Db	541	TTTCCCTCTTATGGCCGATTAATTTGGTTAC	572		

Db	601	ACTTCTTCATCCAGTCAGTAGTACGACAACTTCTGCAAGATGATGTGAGATC	660
Qy	661	ATGCTCTCTTGTGTTCCAAATATATATCTCACCAACGAGGTGTAGGAGTTACA	720
Db	661	ATGCTCTCTTGTGTTCCAAATATATATCTCACCAACGAGGTGTAGGAGTTACA	720
Qy	721	CAAAATAAATGATATGAACTGAAAAGTGAACACTGGGACGAATGGCCAAAGCATCAAC	780
Db	721	CAAAATAAATGATATGAACTGAAAAGTGAACACTGGGACGAATGGCCAAAGCATCAAC	780
Qy	781	TACATCTTCGTGGCCATCTCTGCAATGTGTGTCTTTGTATACGTTTTCTATCTGCT	840
Db	781	TACATCTTCGTGGCCATCTCTGCAATGTGTGTCTTTGTATACGTTTTCTATCTGCT	840
Qy	841	ATCACAAAAGAAAATCTTTAACTGCCACCTTAAGTCAAGTGGAAATCCACTTCGGTCAAA	900
Db	841	ATCACAAAAGAAAATCTTTAACTGCCACCTTAAGTCAAGTGGAAATCCACTTCGGTCAAA	900
Qy	901	AAAGAATCTAGCGCCGACAATATAGAGATCGTGTGTGTGTGTGTGTGTGTGTGTACT	960
Db	901	AAAGAATCTAGCGCCGACAATATAGAGATCGTGTGTGTGTGTGTGTGTGTGTGTACT	960
Qy	961	TACCATATTTGCCAGATCCCTACACAAAAGTGCAGATCGAACCTCATTAACGCTGGCAG	1020
Db	961	TACCATATTTGCCAGATCCCTACACAAAAGTGCAGATCGAACCTCATTAACGCTGGCAG	1020
Qy	1021	TCAAAAGAAATCTTGGCGTATATGAAGAAATTCACCTGTCTATCTGTGCAAAATGA	1080
Db	1021	TCAAAAGAAATCTTGGCGTATATGAAGAAATTCACCTGTCTATCTGTGCAAAATGA	1080
Qy	1081	TGCTTGGACCGCTATATATATATCTTCTATGCGACGCGTTATGGGAAATCTTATGTAAG	1140
Db	1081	TGCTTGGACCGCTATATATATATCTTCTATGCGACGCGTTATGGGAAATCTTATGTAAG	1140
Qy	1141	AAATTCGACATTCCTTAAAGTGCAGAAATGACCTATGACTTCCGAAATCAAAAGAGA	1200
Db	1141	AAATTCGACATTCCTTAAAGTGCAGAAATGACCTATGACTTCCGAAATCAAAAGAGA	1200
Qy	1201	AATACAACTTGAAGACAGATACCTTGTGAGTTCTACCCCTCTCCAAAAGAAAGAC	1260
Db	1201	AATACAACTTGAAGACAGATACCTTGTGAGTTCTACCCCTCTCCAAAAGAAAGAC	1260
Qy	1261	ACGTGTGCATTTGCAATCTTCAATTCATACAAAGAAATCAATAGATATGTGCCCTCAT	1320
Db	1261	ACGTGTGCATTTGCAATCTTCAATTCATACAAAGAAATCAATAGATATGTGCCCTCAT	1320
Qy	1321	CATAAATTCATCTCTAGACCTGCGATCCAAATTAATGTAATTAATTAATTAATTAATTA	1380
Db	1321	CATAAATTCATCTCTAGACCTGCGATCCAAATTAATGTAATTAATTAATTAATTAATTA	1380
Qy	1381	TCGATGCTTTTGTAAACATCAAGAAACATACCCATCAATTAATTCCTAAATCTGAC	1440
Db	1381	TCGATGCTTTTGTAAACATCAAGAAACATACCCATCAATTAATTCCTAAATCTGAC	1440
Qy	1441	CTTCTATCTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1500
Db	1441	CTTCTATCTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1500
Qy	1501	AATAGATTAAGTTATTAACCATAGTCGTGCTAGTAATGTAGAAATTTAAATAGTAAA	1560
Db	1501	AATAGATTAAGTTATTAACCATAGTCGTGCTAGTAATGTAGAAATTTAAATAGTAAA	1560
Qy	1561	TAAACACACATATATCAAGACACTGACTGAGATCTTCTCTCTAAATACAGAA	1620
Db	1561	TAAACACACATATATCAAGACACTGACTGAGATCTTCTCTCTAAATACAGAA	1620
Qy	1621	TCTAGTATGTAATTTGTTTCAACACTGTCCCTTAAGACTTACTTGAAGACGACAGTT	1680
Db	1621	TCTAGTATGTAATTTGTTTCAACACTGTCCCTTAAGACTTACTTGAAGACGACAGTT	1680
Qy	1681	TGATGAAGGGCTAGAGCGTTTGAATTAAGTCAGGTTTTTTCCTGATTTGAAGA	1740
Db	1681	TGATGAAGGGCTAGAGCGTTTGAATTAAGTCAGGTTTTTTCCTGATTTGAAGA	1740

Db	1681	TCGAAAGGGCTAGAGAGCTGTTTGCATAAAAAAGTCAGGTTTTTTTTCCTGATTTGAGA	1740
QY	1741	AGCAGAAAAGCTGACACCCAGCAATCCTTAAGAAAACCCCTTATATATGATATTTGATG	1800
Db	1741	AGCAGAAAAGCTGACACCCAGCAATCCTTAAGAAAACCCCTTATATATGATATTTGATG	1800
QY	1801	GCACTGCAAGGAAGGAGATATTAATTTGATACCTAGCAGAAAATTTTTTTTTCGCA	1860
Db	1801	GCACTGCAAGGAAGGAGATATTAATTTGATACCTAGCAGAAAATTTTTTTTTCGCA	1860
QY	1861	TAGCACTTGAGAGATTTAGATTCACATGCAAAATATGTTTCTCAAAAAGCTAGCTAT	1920
Db	1861	TAGCACTTGAGAGATTTAGATTCACATGCAAAATATGTTTCTCAAAAAGCTAGCTAT	1920
QY	1921	TAAATGACCTGGGGGTTCTGGTGTAGAAATTTTTTAAGTAGGCTTTACTGAGAAACTA	1980
Db	1921	TAAATGACCTGGGGGTTCTGGTGTAGAAATTTTTTAAGTAGGCTTTACTGAGAAACTA	1980
QY	1981	AATTTGGCACTAGGTTATTCAGCACTCCCTGTTCAAATGATATGGCAAAAATTAAGATGA	2040
Db	1981	AATTTGGCACTAGGTTATTCAGCACTCCCTGTTCAAATGATATGGCAAAAATTAAGATGA	2040
QY	2041	CTGGGAAAAAGACACACCCACACCGTAGAACAATATTAATCTACTGGCGAATGGGAAG	2100
Db	2041	CTGGGAAAAAGACACACCCACACCGTAGAACAATATTAATCTACTGGCGAATGGGAAG	2100
QY	2101	GAGACACTTTCTTAAABAAAGCAAAATTAATCTATTTTTTAAATCTAAATTTACATTA	2160
Db	2101	GAGACACTTTCTTAAABAAAGCAAAATTAATCTATTTTTTAAATCTAAATTTACATTA	2160
QY	2161	TGAGTCGAAAATTAACACATTAATAATGAAAATTCACACATCACAATTTTCTGGAAAACGAC	2220
Db	2161	TGAGTCGAAAATTAACACATTAATAATGAAAATTCACACATCACAATTTTCTGGAAAACGAC	2220
QY	2221	GGATTTTACTCTGGAGCATGGCAATGCGATGCGATCTATGAGCTACCAAAACTTAAT	2280
Db	2221	GGATTTTACTCTGGAGCATGGCAATGCGATGCGATCTATGAGCTACCAAAACTTAAT	2280
QY	2281	TCCTTCTCTGCTAATTAACATGCGTAGAAGCACTCATCTATTTTCCAATGTTCTTTGAAA	2340
Db	2281	TCCTTCTCTGCTAATTAACATGCGTAGAAGCACTCATCTATTTTCCAATGTTCTTTGAAA	2340
QY	2341	ACATTTTATTAAGTAATGTTTGTATCTAATTCATGCTTACTGCTATATACATAAAG	2400
Db	2341	ACATTTTATTAAGTAATGTTTGTATCTAATTCATGCTTACTGCTATATACATAAAG	2400
QY	2401	AAATGTTTTAATACG	2416
Db	2401	AAATGTTTTAATACG	2416

for SEQ ID NO: 453

RESULT 3
AW006758
LOCUS AW006758 362 bp mRNA linear EST 08-MAR-2000
DEFINITION wt07a10.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506746 3',
mRNA sequence.
ACCESSION AW006758
VERSION AW006758.1 GI:5855536
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 362)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 442 Std Error: 0.00
Seq primer: -40UP from Gibco.

FEATURES
source Location/Qualifiers
1..362
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2506746"
/clone_lib="NCI_CGAP_Co3"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from 12 pooled bulk tumor samples and primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library went through one round of
normalization."

BASE COUNT 82 a 93 c 91 g 96 t
ORIGIN

Query Match 100.0%; Score 330; DB 10; Length 362;
Best Local Similarity 100.0%; Pred. No. 6.3e-89;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGGATAAATATATTAGCAAATAAATATATTTCTTAACATAGTGCCTGATTCAAGCGTC 60
|||||
Db 1 TGTGGATAAATATATTAGCAAATAAATATATTTCTTAACATAGTGCCTGATTCAAGCGTC 60
QY 61 TGTCTGGTTCAGATATAAATACCCATGTGGGTACCTAGGTGCTAGTCTCCCACTAACTG 120
|||||
Db 61 TGTCTGGTTCAGATATAAATACCCATGTGGGTACCTAGGTGCTAGTCTCCCACTAACTG 120
QY 121 AGGGAAAAAGGTTCCCAAGGTGGGTCCTCTGCCCACCTTTGCCACCACATTACATTTCCAA 180
|||||
Db 121 AGGGAAAAAGGTTCCCAAGGTGGGTCCTCTGCCCACCTTTGCCACCACATTACATTTCCAA 180
QY 181 ATGGGATAATGCCTGAGGGGCCAAGAGTGGTCAGGCTGCCCTGGGGTGAATGTCAACCTG 240
|||||
Db 181 ATGGGATAATGCCTGAGGGGCCAAGAGTGGTCAGGCTGCCCTGGGGTGAATGTCAACCTG 240
QY 241 ATGAGGCCCATCAGCTCTTGTCCTCAGTGAGGCCAGACTTGTGCTCTAATCCACTCTC 300
|||||
Db 241 ATGAGGCCCATCAGCTCTTGTCCTCAGTGAGGCCAGACTTGTGCTCTAATCCACTCTC 300
QY 301 CTGTGGGTCCCTGGCCTGTATGGCTTATAC 330
|||||
Db 301 CTGTGGGTCCCTGGCCTGTATGGCTTATAC 330

RESULT 4

ABV29346

ID ABV29346 standard; cDNA; 734 BP.

XX

AC ABV29346;

XX

DT 16-SEP-2002 (first entry)

XX

DE Human prostate expression marker cDNA 29337.

XX

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200160860-A2.

XX

PD 23-AUG-2001.

XX

PF 20-FEB-2001; 2001WO-US05171.

XX

PR 17-FEB-2000; 2000US-183319P.

PR

PR 16-MAR-2000; 2000US-189862P.

PR

PR 25-MAY-2000; 2000US-207454P.

PR

PR 09-JUN-2000; 2000US-211314P.

PR

PR 18-JUL-2000; 2000US-219007P.

PR

PR 13-DEC-2000; 2000US-255281P.

XX

PA

XX

PI

XX

DR

XX

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Sequence 734 BP; 193 A; 157 C; 114 G; 218 T; 52 other;

Query Match 100.0%; Score 320; DB 23; Length 734;
Best Local Similarity 100.0%; Pred. NO. 1.1e-82;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGTGGCAGATTTTCTTTAATAGATATATTTCAAACAGATACAACAAATTAATAATC 60
DB 93 CACAGTGGCAGATTTTCTTTAATAGATATATTTCAAACAGATACAACAAATTAATAATC 152
QY 61 TAATTCACGGCAGGTAAACATGGGTGCTCAAAAAGTTCCACATAGACATTACACTTGGG 120
DB 153 TAATTCACGGCAGGTAAACATGGGTGCTCAAAAAGTTCCACATAGACATTACACTTGGG 212
QY 121 CCATCAGTATTTCCTTCACATTCCTTTTGTAAAGTCCCATCTTCGCAGTGGCAGTACAG 180
DB 213 CCATCAGTATTTCCTTCACATTCCTTTTGTAAAGTCCCATCTTCGCAGTGGCAGTACAG 272
QY 181 GAGAAATCTCCACCGTCACCGCACAATCCACAGGCGCATTACCACCTGAAGTGAAGGC 240
DB 273 GAGAAATCTCCACCGTCACCGCACAATCCACAGGCGCATTACCACCTGAAGTGAAGGC 332
QY 241 TCATCTCGAAGGTGCGCTCAGCCATAAAAAGAAAACATATTACAGAAAGGAAAAATAAGT 300
DB 333 TCATCTCGAAGGTGCGCTCAGCCATAAAAAGAAAACATATTACAGAAAGGAAAAATAAGT 392
QY 301 GTGCTCTTCCACCGCAA 320
DB 393 GTGCTCTTCCACCGCAA 412

RESULT 4
AI368176
LOCUS AI368176 392 bp mRNA linear EST 13-FEB-1999
DEFINITION qk65b10.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1873819 3',
mRNA sequence.
ACCESSION AI368176
VERSION AI368176.1 GI:4137921
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 392)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1195 Std Error: 0.00
Seq primer: -40UP from GIBCO
High quality sequence stop: 381.

FEATURES
source Location/Qualifiers
1..392
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1873819"
/clone_lib="NCI_CGAP_Co8"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."

BASE COUNT 121 a 102 c 65 g 104 t
ORIGIN

Query Match 100.0%; Score 320; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 8.6e-66;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGTGGCAGATTTTCTTTAATAGATATATTTCAAACAGATACAACAAATTAATAATC 60
|||||
Db 6 CACAGTGGCAGATTTTCTTTAATAGATATATTTCAAACAGATACAACAAATTAATAATC 65

QY 61 TAATTCACGGCAGGTAAACATGGGTGCTCAAAAAGTTCCACATAGACATTTACACTTGGG 120
|||||
Db 66 TAATTCACGGCAGGTAAACATGGGTGCTCAAAAAGTTCCACATAGACATTTACACTTGGG 125

QY 121 CCATCAGTATTTCCCTCACATTCCTTTTGTTAAGTCCCATCTTCGCAGTGGCAGTACAG 180
|||||
Db 126 CCATCAGTATTTCCCTCACATTCCTTTTGTTAAGTCCCATCTTCGCAGTGGCAGTACAG 185

QY 181 GAGAAATCTCCACCGTCACCGCACAATCCACCGGCGCATTACCACCTGAAGTGAAGGTC 240
|||||
Db 186 GAGAAATCTCCACCGTCACCGCACAATCCACCGGCGCATTACCACCTGAAGTGAAGGTC 245

QY 241 TCATCTCGAAGGTGCGCTCAGCCATAAAAAGAAAACATATTACAGAAAGGAAAAATAAGT 300
|||||
Db 246 TCATCTCGAAGGTGCGCTCAGCCATAAAAAGAAAACATATTACAGAAAGGAAAAATAAGT 305

QY 301 GTGCTCTTCCACCGCAAA 320
|||||
Db 306 GTGCTCTTCCACCGCAAA 325

[illegible]

RESULT 4
HOMOXYPLA 1971 bp mRNA linear PRI 29-MAY-2002
LOCUS Homo sapiens mRNA for cytochrome P-450 HPLA, complete cds.
DEFINITION
ACCESSION D00408.1 GI:220148
VERSION
KEYWORDS CYP3A6; cytochrome P-450; human fetal liver cytochrome P-450.
SOURCE Homo sapiens fetus liver cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1971)

REFERENCE
AUTHORS Komori, M., Nishio, K., Oh, H., Kitada, M. and Kamataki, T.
TITLE Molecular cloning and sequence analysis of cDNA containing the
entire coding region for human fetal liver cytochrome P-450
J. Biochem. 105 (2), 161-163 (1989)
MEDLINE 89255154
COMMENT Submitted in computer readable form by M. Komori on 15-Apr-1989.
The deduced N-terminal amino acid sequence was identical to that of
P-450 HPLA.

FEATURES

location/Qualifiers

1..1971
/organism="Homo sapiens"
/db_xref="taxon:9606"
/issue_type="liver"
/dev_stage="fetus"
/note="106 bp upstream of HindIII site.-clones
lambda-HPL33, lambda-HPL10"
4..1515
/product="cytochrome P-450 HPLA"
/protein_id="BA00310.1"
/db_xref="GI:220149"
/translation="MDLIPMLAVETWLLAVSLILYLSTRHGLFKLIGPEPPL
PTGNALSPKGTWTFDMCYKTRKRWGIIYDQOPLATTDPMITVYKCYSTF
TNRPEPVGFNNAISIADEEMKRIKSLSPFTSGKIKENVPILAOYGDVLRNL
RRAELEGKPTLKHVFGAYSNVITSFVSIIDSLNPDQPVENKRLIRPNLDP
FVLSIKYPLPLTFLVGNLITVPKRVISFTSKSVKQIKERKLNKQKHVDPLQIM
DSQNSKDSFTKHALSDLEMAOSIIFPAAGERTSSVLSIIYELATHRPVQOAKGE
IDVYLPKAPPTDYVQLETILMAYNEIIRLFPAAKLRCKDKVDINGMTIPKGV
VMIPTVLAHDPKWTPEPKFLPERSKKNQNDIDYIITPGSGPRNCIGRFAVY

CDS
1..1971
/product="cytochrome P-450 HPLA"
/protein_id="BA00310.1"
/db_xref="GI:220149"
/translation="MDLIPMLAVETWLLAVSLILYLSTRHGLFKLIGPEPPL
PTGNALSPKGTWTFDMCYKTRKRWGIIYDQOPLATTDPMITVYKCYSTF
TNRPEPVGFNNAISIADEEMKRIKSLSPFTSGKIKENVPILAOYGDVLRNL
RRAELEGKPTLKHVFGAYSNVITSFVSIIDSLNPDQPVENKRLIRPNLDP
FVLSIKYPLPLTFLVGNLITVPKRVISFTSKSVKQIKERKLNKQKHVDPLQIM
DSQNSKDSFTKHALSDLEMAOSIIFPAAGERTSSVLSIIYELATHRPVQOAKGE
IDVYLPKAPPTDYVQLETILMAYNEIIRLFPAAKLRCKDKVDINGMTIPKGV
VMIPTVLAHDPKWTPEPKFLPERSKKNQNDIDYIITPGSGPRNCIGRFAVY

BASE COUNT 597 a 428 c 397 g 549 t
ORIGIN
Query Match 100.0%; Score 1971; DB 9; Length 1971;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1971; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
NKKLIVRLVNLNFSKPKCKEIOIPKILRFGILLTEKPIVLKASRDETIVGSA*
QY 1 GTATGATCTCATCCCAAACTTGGCCGAGAAACCGGCTTCCTGGCTGCAAGC 60
DB 1 GTATGATCTCATCCCAAACTTGGCCGAGAAACCGGCTTCCTGGCTGCAAGC 60
QY 61 ATACTCCTATCTATATGGAACCCGTACACATGACTTTTAAAGAGCTTGAATCCA 120
DB 61 ATACTCCTATCTATATGGAACCCGTACACATGACTTTTAAAGAGCTTGAATCCA 120
QY 121 GGGCCCAACACCTCTGCTTTTGGAAATGCTTGTCTTCCTAAGGCGCTATGGAG 180
DB 121 GGGCCCAACACCTCTGCTTTTGGAAATGCTTGTCTTCCTAAGGCGCTATGGAG 180
QY 181 TTGACATGGAATGTATATAAAGTATAGAAAGTCTGGGATTTATGACTGTCAACAG 240
DB 181 TTGACATGGAATGTATATAAAGTATAGAAAGTCTGGGATTTATGACTGTCAACAG 240
QY 241 CCTATGCTGGCTATCACAGATCCCGACATGATCAAAACAGTGTAGTGAAGATGTAT 300
DB 241 CCTATGCTGGCTATCACAGATCCCGACATGATCAAAACAGTGTAGTGAAGATGTAT 300
QY 301 TCTGTCTTCACAAACCGGAGGCTTTTCGGCCAGTGGGATTTAGAAAAATGCCATCT 360
DB 301 TCTGTCTTCACAAACCGGAGGCTTTTCGGCCAGTGGGATTTAGAAAAATGCCATCT 360
QY 361 ATAGCTGAGATGAGAATGGAAGAGATACATGATGCTGTCCCAATTCACAGC 420
DB 361 ATAGCTGAGATGAGAATGGAAGAGATACATGATGCTGTCCCAATTCACAGC 420
QY 421 GGAACCTCAAGAGATGTCCTTATCCCATGTCACAGTATGAGATGTGTGTGAGAAAT 480
DB 421 GGAACCTCAAGAGATGTCCTTATCCCATGTCACAGTATGAGATGTGTGTGAGAAAT 480
QY 481 CTGAGGGGAGACGAGAGACAGGACAGCCCTGTCACTTGAACAGCTTTGGGCGCTAC 540
DB 481 CTGAGGGGAGACGAGAGACAGGACAGCCCTGTCACTTGAACAGCTTTGGGCGCTAC 540
QY 541 AGCATGATGTGATACATACATCATCTTTGAGTGAATGCACTGTCACAAATCCA 600
DB 541 AGCATGATGTGATACATACATCATCTTTGAGTGAATGCACTGTCACAAATCCA 600
QY 601 CAAGACCCCTTTGTGAAACACCCAGAGACCTTTTAAGATTATTCATTAGATCATTC 660
DB 601 CAAGACCCCTTTGTGAAACACCCAGAGACCTTTTAAGATTATTCATTAGATCATTC 660
QY 661 GTTCTCATTAAGAGCTTTCCATCTTCAACCAATTTCTTGAAGCATTAATATCACT 720
DB 661 GTTCTCATTAAGAGCTTTCCATCTTCAACCAATTTCTTGAAGCATTAATATCACT 720
QY 721 GTGTTTCAAGAAAGTATTAAGTTTCTAACAACCTGTAACAGATTAAGAAAGCT 780
DB 721 GTGTTTCAAGAAAGTATTAAGTTTCTAACAACCTGTAACAGATTAAGAAAGCT 780
QY 781 CGGCTCAAGAGACACAAAGACACAGAGTATTCCTTACAGTATGATGACTCTCAG 840
DB 781 CGGCTCAAGAGACACAAAGACACAGAGTATTCCTTACAGTATGATGACTCTCAG 840
QY 841 AATTCAAAAGACTGTGAGACCAACAAAGCTGTGATGTGAGACTCATGAGCCCAATCA 900
DB 841 AATTCAAAAGACTGTGAGACCAACAAAGCTGTGATGTGAGACTCATGAGCCCAATCA 900
QY 901 AATATCTTTATTTTGTGCTATGAAACACAGAGAGTGTCTCTCTCATATATAT 960
DB 901 AATATCTTTATTTTGTGCTATGAAACACAGAGAGTGTCTCTCTCATATATAT 960
QY 961 GAACCTGCACACCTGATGTCCAGACAGAAAGTGCAGAAAGAAATGATACAGTTTA 1020

- continuation -

For SEQ ID NO: 651

Wed Jun 4 11:54:11 2003

us-09-873-3

```
Db 961 |||||GAAGTGGCCACTCACCTGATGTCCAGCAGAAAGTGCAGAAGGAAATTGATACAGTTT||| 1020
Qy 1021 CCCAATAAGGCACCCACCCACCTATGATACTGTGCTACAGTTGGAGTATCTTGACATGGTG 1080
Db 1021 CCCAATAAGGCACCCACCCACCTATGATACTGTGCTACAGTTGGAGTATCTTGACATGGTG 1080
Qy 1081 GTGAATGAAACACTCAGATTATTCAGTTGCTATGAGACTTGAGAGGGTCTGCAAAAAA 1140
Db 1081 GTGAATGAAACACTCAGATTATTCAGTTGCTATGAGACTTGAGAGGGTCTGCAAAAAA 1140
Qy 1141 GATGTTGAAATCAATGGGATGTTTATTCCTAAAGGGTGGTGGTATGATTCCAAGCTAT 1200
Db 1141 GATGTTGAAATCAATGGGATGTTTATTCCTAAAGGGTGGTGGTATGATTCCAAGCTAT 1200
Qy 1201 GTTCTTCATCATGACCCAAAGTACTGGACAGAGCCTGAGAAGTTCTCCCTGAAAGGTTTC 1260
Db 1201 GTTCTTCATCATGACCCAAAGTACTGGACAGAGCCTGAGAAGTTCTCCCTGAAAGGTTTC 1260
Qy 1261 AGTAAAAAGAACCAAGGACAACATAGATCCTTACATATACACACCCCTTTGGAAGTGGACCC 1320
Db 1261 AGTAAAAAGAACCAAGGACAACATAGATCCTTACATATACACACCCCTTTGGAAGTGGACCC 1320
Qy 1321 AGAAACTGCATTGGCATGAGGTTTGCTCTCGTGAACATGAAACTTGCTCTAGTCAGAGTC 1380
Db 1321 AGAAACTGCATTGGCATGAGGTTTGCTCTCGTGAACATGAAACTTGCTCTAGTCAGAGTC 1380
Qy 1381 CTTCAGAACTTCTCCTTCAAACCTTGTAAGAAACACAGATCCCCCTGAAATTACGCTTT 1440
Db 1381 CTTCAGAACTTCTCCTTCAAACCTTGTAAGAAACACAGATCCCCCTGAAATTACGCTTT 1440
Qy 1441 GGAGGACTTCTTCTAACAGAAAAACCCATTGTTCTAAAGGCTGAGTCAAGGGATGAGACC 1500
Db 1441 GGAGGACTTCTTCTAACAGAAAAACCCATTGTTCTAAAGGCTGAGTCAAGGGATGAGACC 1500
Qy 1501 GTAAGTGGAGCCTGATTTCCTAAGGACTTCTGGTTTGCTCTTTAAGAAAGCTGTGCCCC 1560
Db 1501 GTAAGTGGAGCCTGATTTCCTAAGGACTTCTGGTTTGCTCTTTAAGAAAGCTGTGCCCC 1560
Qy 1561 AGAACACCAGAGACCTCAAATTACTTTACAAATAGAACCCTGAAATGAAGACGGGCTTCA 1620
Db 1561 AGAACACCAGAGACCTCAAATTACTTTACAAATAGAACCCTGAAATGAAGACGGGCTTCA 1620
Qy 1621 TCCAATGTGCTGCATAAATAATCAGGGATTCTGTACGTGCATTGTGCTCTCTCATGGTCT 1680
Db 1621 TCCAATGTGCTGCATAAATAATCAGGGATTCTGTACGTGCATTGTGCTCTCTCATGGTCT 1680
Qy 1681 GTATAGAGTGTATAGTGGTAATATAGAGGAGATGACCAAATCAGTGTGGGGAAGTAG 1740
Db 1681 GTATAGAGTGTATAGTGGTAATATAGAGGAGATGACCAAATCAGTGTGGGGAAGTAG 1740
Qy 1741 ATTTGGCTTCTCTGCTTCTCATAGGACTATCTCCACCACCCCAAGTTAGCACCATTAACT 1800
Db 1741 ATTTGGCTTCTCTGCTTCTCATAGGACTATCTCCACCACCCCAAGTTAGCACCATTAACT 1800
Qy 1801 CCTCCTGAGCTCTGATAACATAATTAACATTCTCAATAATTTCAACCACAATCATTAA 1860
Db 1801 CCTCCTGAGCTCTGATAACATAATTAACATTCTCAATAATTTCAACCACAATCATTAA 1860
Qy 1861 AAAAAATAGGAATTATTTGATGGCTCTAACAGTGACATTTATATCATGTGTTATATCTGT 1920
Db 1861 AAAAAATAGGAATTATTTGATGGCTCTAACAGTGACATTTATATCATGTGTTATATCTGT 1920
Qy 1921 AGTATTCTATAGTAAGCTTTATATTAAGCAAATCAATAAAACCTCTTTAC 1971
Db 1921 AGTATTCTATAGTAAGCTTTATATTAAGCAAATCAATAAAACCTCTTTAC 1971
```

RESULT 2
 AW967166/c
 LOCUS AW967166 659 bp mRNA linear EST 01-JUN-2000
 DEFINITION EST379240 MAGE resequences, MAGJ Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW967166
 VERSION AW967166.1 GI:8157002
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

SEQ ID NO: 865

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 659)
 AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and Quackenbush, J.
 TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
 JOURNAL Unpublished (2000)
 COMMENT Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@tigr.org
 Plate: 237
 Seq primer: Reverse.

FEATURES
 source Location/Qualifiers
 1..659
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="MAGE resequences, MAGJ"
 /note="Vector: pBluescriptSKm"
 BASE COUNT 213 a 125 c 148 g 173 t
 ORIGIN

Query Match 92.3%; Score 389.6; DB 10; Length 659;
 Best Local Similarity 95.3%; Pred. No. 3.4e-72;
 Matches 403; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 1 TGTTTTTTTNGTATTCTCATGTATACTTCATTATTTTATTAATNANCAANCCCTGT 60
 Db 455 TTTTTTCTGGTATTCTCATGTATACTTCATTATTTTATTAATAAGCAAAGCCCTGT 396
 QY 61 AAGGGANTNCTTGCCTAGTCNTCCGACTNTGNTTNATCTTCATCTTGACTAATCNGGAA 120
 Db 395 AAGGGAGCCCTTGCCTAGTCCTCCGACTCTGATTTCATCTTCATCTTGACTAATCTGGAA 336
 QY 121 GTAACNAAG-TCGTAGGTCTCCTTGTCAGATGCAANCANTCGAAGCCAATCACGAAGATT 179
 Db 335 GTAACGAAGTTCGTAGGTCTCCTTGTCAGATGCAACCACTCGAAGCCAATCACGAAGATT 276
 QY 180 GTTCTTCTTAAGGTATTCTTGGTAAGGTATTTCAAATACCTTTTAGAGAAGTGTTCCTC 239
 Db 275 GTTCTTCTTAAGGTATTCTTGGTAAGGTATTTCAAATACCTTTTAGAGAAGTGTTCCTC 216
 QY 240 AGAAACAAGTGTGATTTTATTCTTGAAGCGTTCAATGTGAACAACATTCCTGAGATTTC 299
 Db 215 AGAAACAAGTGTGATTTTATTCTTGAAGCGTTCAATGTGAACAACATTCCTGAGATTTC 156
 QY 300 AGTTTGGCCATTGACTTTAACCTTCTCCCGTAGAAATGCTCAAAATTTCCAGAATCAAA 359
 Db 155 AGTTTGGCCATTGACTTTAACCTTCTCCCGTAGAAATGCTCAAAATTTCCAGAATCAAA 96
 QY 360 AATCCATCTTCTACTGGATGAGTAAGGTCCAAATTAAACCTCCAGGTTGACCTCTTGGG 419
 Db 95 AATCCATCTTCTACTGGATGAGTAAGGTCCAAATTAAACCTCCAGGTTGACCTCTTGGG 36
 QY 420 CTT 422
 Db 35 CTT 33

ALIGNMENTS

Seq ID No: 1015

RESULT 1
 N22479
 LOCUS N22479 354 bp mRNA linear EST 20-DEC-1995
 DEFINITION yw35a11.s1 Morton Fetal Cochlea Homo sapiens cDNA clone
 IMAGE:254204 3', mRNA sequence.
 ACCESSION N22479
 VERSION N22479.1 GI:1128613
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 354)
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
 Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
 TITLE Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL Genome Res. 6 (9), 807-828 (1996)
 MEDLINE 97044478
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 268

Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 484 Std Error: 0.00
 Seq primer: ml3 -40 forward
 High quality sequence stop: 268.

FEATURES
 source
 Location/Qualifiers
 1..354
 /organism="Homo sapiens"
 /db_xref="GDB:3891657"
 /db_xref="taxon:9606"
 /clone="IMAGE:254204"
 /clone_lib="Morton Fetal Cochlea"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: ear; Vector: pBluescript SK-; Site_1: EcoRI;
 Site_2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo dt. Fetal cochlea, normal.
 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTT 3'"

BASE COUNT 120 a 68 c 37 g 129 t
 ORIGIN
 Query Match 100.0%; Score 354; DB 14; Length 354;
 Best Local Similarity 100.0%; Pred. No. 1.3e-46;
 Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTTTTTTTTTTTTTGTTCATATCCATAAAGTTTATTTTAAAAAACTGTTAAAAACTAA 60
 Db 1 TTTTTTTTTTTTTTTTGTTCATATCCATAAAGTTTATTTTAAAAAACTGTTAAAAACTAA 60
 QY 61 CCATACAGGTTTATTAATATACTTAAAAAGTTTGTTCCTATGTTGAAGTAAATACATT 120
 Db 61 CCATACAGGTTTATTAATATACTTAAAAAGTTTGTTCCTATGTTGAAGTAAATACATT 120
 QY 121 AGCAACATCTCCGGACACCATCTTTATAAAAGTAAAACTTCTAGATCCTGAAATGTACT 180
 Db 121 AGCAACATCTCCGGACACCATCTTTATAAAAGTAAAACTTCTAGATCCTGAAATGTACT 180
 QY 181 ACAGTAGAGTCTATAGTTTACACTTTTAATCACAGATTGGAATTCATTCTCCTTACTCCC 240
 Db 181 ACAGTAGAGTCTATAGTTTACACTTTTAATCACAGATTGGAATTCATTCTCCTTACTCCC 240
 QY 241 CTACTTCCCACATGTGGCAGTTTATTACTTCAAAATTAATGACATTCACTCATGTTATACT 300
 Db 241 CTACTTCCCACATGTGGCAGTTTATTACTTCAAAATTAATGACATTCACTCATGTTATACT 300
 QY 301 ACCACAGATCCTTAAATAGAGTACATACTGCATAATTACTAACAGAGCCAGTCT 354
 Db 301 ACCACAGATCCTTAAATAGAGTACATACTGCATAATTACTAACAGAGCCAGTCT 354

RESULT 4
AAZ51562/c
ID AAZ51562 standard; cDNA; 580 BP.
XX
AC AAZ51562;
XX
DT 21-JUN-2000 (first entry)
XX
DE Human hypoxia response regulating gene, 77H4 related cDNA clone 18E.
XX
KW Hypoxia response regulating gene; gene 77H4; human; EST 18E; cardiant;
KW apoptosis; angiogenesis; vasotropic; cytostatic; ophthalmological;
KW cerebroprotective; antagonist; regulator; inhibitor; treatment; tumour;
KW hypoxia associated pathology; HAP; gene therapy; diagnosis; ischaemia;
KW steroid receptor coactivator; SRA; retinopathy; myocardial infarction;
KW stroke; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT polyA_signal 536..541
FT /*tag= a
XX
PN WO200012525-A1.
XX
PD 09-MAR-2000.
XX
PF 27-AUG-1999; 99WO-US20394.
XX
PR 27-AUG-1998; 98US-0098158.
PR 05-MAY-1999; 99US-0132684.
XX
PA (QUAR-) QUARK BIOTECH INC.
PA (KOHN/) KOHN K.
XX
PI Einat P, Skaliter R, Feinstein E;
XX
DR WPI; 2000-256577/22.
XX
PT Novel polynucleotides capable of regulating angiogenesis or apoptosis
PT useful for diagnosis and treatment of hypoxia, ischemia and tumor
XX
PS growth -
XX
Claim 1; Fig 7a; 78pp; English.
XX
CC The present sequence is the human hypoxia response regulating gene,
CC 77H4, related cDNA clone 18E. The gene 77H4 has similarity to steroid
CC receptor transcriptional co-activator, SRA function and can serve as
CC a coactivator in some transcriptional complexes. It has vasotropic,
CC cardiant, ophthalmological, cytostatic and cerebroprotective activity.
CC Antagonist of the encoded protein, functions as a regulator of apoptosis
CC or angiogenesis. The protein encoded by this polynucleotide, the
CC biologically active product from enzymatic activity of the protein or
CC inhibitor of the enzymatic activity is useful for regulating hypoxia
CC associated pathologies (HAP). It is useful for gene therapy, diagnosis
CC and treatment of tumour growth and ischaemia, e.g., retinopathy,
CC myocardial infarction and stroke.
XX
SQ Sequence 580 BP; 177 A; 111 C; 134 G; 158 T; 0 other;

Query Match 97.5%; Score 428; DB 21; Length 580;
Best Local Similarity 99.8%; Pred. No. 1.3e-125;
Matches 439; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTTTGGATTTAAAGATTTTATTTCTTTATGCAGGTAGGCAGTTAGAAATTTCAAAGTC 60
Db 558 TTTTGGATTTAAAGATTTTATTTCTTTATGCAGGTAGGCAGTTAGAAATTTCAAAGTC 499
QY 61 TAACAATGACATTCTTGAAGTGGGCACAG-CTTTAAACTCAGGCTATGTATACAGTAAC 119
Db 498 TAACAATGACATTCTTGAAGTGGGCACAGCCTTTAAACTCAGGCTATGTATACAGTAAC 439
QY 120 CTTGTGGAAGTGGTTCAGCCAGATCTTCACTTTTCATGAAAGCACAGGCTCTGTCTTTTC 179
Db 438 CTTGTGGAAGTGGTTCAGCCAGATCTTCACTTTTCATGAAAGCACAGGCTCTGTCTTTTC 379
QY 180 TTTCCAGAGGGCTCCTCTCATATTTCCATCGCCAGTTTCTGTTACAAGGCAGACTGAATCA 239
Db 378 TTTCCAGAGGGCTCCTCTCATATTTCCATCGCCAGTTTCTGTTACAAGGCAGACTGAATCA 319
QY 240 AGCCAAGATCAACACACACTGGTACACGTGGCTCCCAACCAATTTTATATGTATATATAT 299
Db 318 AGCCAAGATCAACACACACTGGTACACGTGGCTCCCAACCAATTTTATATGTATATATAT 259
QY 300 ATTCTACTTCCAACACCCGATTCATCTGTTCAATCAAAGCCTGGTTTGGCCAACAA 359
Db 258 ATTCTACTTCCAACACCCGATTCATCTGTTCAATCAAAGCCTGGTTTGGCCAACAA 199
QY 360 TAAACTCGTCAGGAGATCGAAGGTTGTAGATGTCTGCACGTGGCTTCTTGGAGGTCCAG 419
Db 198 TAAACTCGTCAGGAGATCGAAGGTTGTAGATGTCTGCACGTGGCTTCTTGGAGGTCCAG 139
QY 420 TGGTGACTCCCTCTTCCAAA 439
Db 138 TGGTGACTCCCTCTTCCAAA 119

RESULT 1
 N98464
 LOCUS N98464 439 bp mRNA linear EST 20-AUG-1996
 DEFINITION zb86b06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
 clone IMAGE:310451 3', mRNA sequence.
 ACCESSION N98464
 VERSION N98464.1 GI:1269909
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 439)
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
 Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
 TITLE Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL Genome Res. 6 (9), 807-828 (1996)
 MEDLINE 97044478
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 568 Std Error: 0.00
 Seq primer: mob.REGA+ET
 High quality sequence stop: 377.

FEATURES
 source Location/Qualifiers
 1..439
 /organism="Homo sapiens"
 /db_xref="GDB:1253865"
 /db_xref="taxon:9606"
 /clone="IMAGE:310451"
 /clone_lib="Soares_senescent_fibroblasts_NbHSF"
 /tissue_type="senescent fibroblast"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Vector: pT7T3D (Pharmacia) with a modified
 polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
 ; 1st strand cDNA was primed with a Not I - oligo(dT)
 primer [5'
 TGTACCAATCTGAAGTGGGAGCGCGCATTTTTTTTTTTTTTTTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot - 5. Library constructed by Bento
 Soares and M.Fatima Bonalga."
 BASE COUNT 118 a 101 c 83 g 137 t
 ORIGIN

Query Match 100.0%; Score 439; DB 14; Length 439;
 Best Local Similarity 100.0%; Pred. No. 1.1e-110;
 Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTAAAGATTTTATTTCTTTATGCAGGTAGGCAGTTAGAAATTTCAAAGTC 60
 Db 1 TTTTGATTAAAGATTTTATTTCTTTATGCAGGTAGGCAGTTAGAAATTTCAAAGTC 60
 QY 61 TAACAATGACATTCTTGAAGTGGGCACAGCTTTTAACTCAGGCTATGTATACAGTAACC 120
 Db 61 TAACAATGACATTCTTGAAGTGGGCACAGCTTTTAACTCAGGCTATGTATACAGTAACC 120
 QY 121 TTGTGGAAGTGGTTCAGCCAGATCTTCACTTTTCATGAAAGCACAGGCTGTGCTCTTTCT 180
 Db 121 TTGTGGAAGTGGTTCAGCCAGATCTTCACTTTTCATGAAAGCACAGGCTGTGCTCTTTCT 180
 QY 181 TTCCAGAGGGCTCCTCTCATATCCATCGCCAGTTTCTGTTACAAGGCAGACTGAATCAA 240
 Db 181 TTCCAGAGGGCTCCTCTCATATCCATCGCCAGTTTCTGTTACAAGGCAGACTGAATCAA 240
 QY 241 GCCAAGATCAACACACACTGGTACACGTGGCTCCCAACCAATTTTATATGTATATATATA 300
 Db 241 GCCAAGATCAACACACACTGGTACACGTGGCTCCCAACCAATTTTATATGTATATATATA 300
 QY 301 TTCTACTTCCAACACCCGCATTTCCTGGTTCAATCAAAGCCTGGTTTGGCCAAACAT 360
 Db 301 TTCTACTTCCAACACCCGCATTTCCTGGTTCAATCAAAGCCTGGTTTGGCCAAACAT 360
 QY 361 AAACCTCGTCAGGAGATCGAAGGTTGTAGATGTCTGCACGTGGCTTCCTTGGAGGTCCAGT 420
 Db 361 AAACCTCGTCAGGAGATCGAAGGTTGTAGATGTCTGCACGTGGCTTCCTTGGAGGTCCAGT 420
 QY 421 GGTGACTCCCTCTTCCAAA 439
 Db 421 GGTGACTCCCTCTTCCAAA 439

RESULT 1
W90146
LOCUS W90146 304 bp mRNA linear EST 07-MAY-1997
DEFINITION zh75e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
clone IMAGE:417916 3', mRNA sequence.
ACCESSION W90146
VERSION W90146.1 GI:1406136
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 304)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissos, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins,
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1214 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 267.

FEATURES
source
Location/Qualifiers
1..304
/organism="Homo sapiens"
/db_xref="GDB:1326386"
/db_xref="taxon:9606"
/clone="IMAGE:417916"
/clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen 1NFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer. [5'
AACTGGAAGAATTAATAAGATCTTTTTTTTTTTTTTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 86 a 72 c 45 g 100 t 1 others
ORIGIN
Query Match 99.7%; Score 303; DB 14; Length 304;
Best Local Similarity 100.0%; Pred. No. 5e-75;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CACTTATAGCCAATATTTAATAATCCCATATTAAGTGTGTAATAAATGTCTTTATGA	60
Db	1	CACTTATAGCCAATATTTAATAATCCCATATTAAGTGTGTAATAAATGTCTTTATGA	60
Qy	61	TCTGTTACCAACCAAAAGATGCATCATAACTTTCAAGANTATGTTCTTTGACTTCTAAC	120
Db	61	TCTGTTACCAACCAAAAGATGCATCATAACTTTCAAGANTATGTTCTTTGACTTCTAAC	120
Qy	121	CTCTGCTCTTCTTTAGAAATTACCTTTGCTGCGGCCAGTACATGCTCCTTGTAAATGACTC	180
Db	121	CTCTGCTCTTCTTTAGAAATTACCTTTGCTGCGGCCAGTACATGCTCCTTGTAAATGACTC	180
Qy	181	TACATTTACTCGCACAAAGCGTTTGTCTGGAAGTCTTCTGCTAATCGATGAACAAACAGTA	240
Db	181	TACATTTACTCGCACAAAGCGTTTGTCTGGAAGTCTTCTGCTAATCGATGAACAAACAGTA	240
Qy	241	AACAGTTTCAGATGGACCAATAAGTCACCACTTTTCTCCAGACCGAAGTTGGAGGGCTTCT	300
Db	241	AACAGTTTCAGATGGACCAATAAGTCACCACTTTTCTCCAGACCGAAGTTGGAGGGCTTCT	300
Qy	301	TTCC 304	
Db	301	TTCC 304	